SEQUENCE LISTING

<110> Max-Planck-Gesellschaft zur Förderung der Wissensc

<120> L-amino acid oxidase with cytotoxic activity from Aplysia punctata

<130> 29644PWO_2

<140> PCT/EP04/00423
<141> 2004-01-20

<150> EP03001232.2
<151> 2003-01-20

<150> EP03026613.4
<151> 2003-11-19

<160> 72

<170> PatentIn Ver. 2.1

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cac gcc gac ggt atc tgc aga aac aga cgt caa tgt aac aga gag gtg   96
His Ala Asp Gly Ile Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val
             20                  25                  30

tgc ggt tct acc tac gat gtg gcc gtc gtg ggg gcg ggg cct ggg gga   144
Cys Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly
         35                  40                  45

gct aac tcc gcc tac atg ctg agg gac tcc ggc ctg gac atc gct gtg   192
Ala Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val
     50                  55                  60

ttc gag tac tcg gac cga gtg ggc ggc cgg ctg ttc acc tac cag ctg   240
Phe Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu
 65                  70                  75                  80

ccc aac aca ccc gac gtt aac ctg gag att ggc ggc atg agg ttc atc   288
Pro Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile
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gaa ggc gcc atg cac agg ctc tgg agg gtc att tca gaa ctc ggc cta   336
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Glu Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu
            100                 105                 110

acc ccc aag gtg ttc aag gaa ggt ttc ggc aag gag ggc aga caa aga   384
Thr Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg
        115                 120                 125

ttt tac ctg cgg gga cag agc ctg acc aag aaa cag gtc aag agt ggg   432
Phe Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly
    130                 135                 140

gac gta ccc tat gac ctc agc ccg gag gag aaa gaa aac cag gga aat   480
Asp Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn
145                 150                 155                 160

ctg gtc gaa tac tac ctg gag aaa ctg aca ggt cta caa ctc aac ggc   528
Leu Val Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Gln Leu Asn Gly
                165                 170                 175

gag ccg ctc aaa cgt gag gtt gcg ctt aaa cta acc gtg ccg gac ggc   576
Glu Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly
            180                 185                 190

aga ttc ctc tat gac ctc tcg ttt gac gaa gcc atg gat ctg gtt gcc   624
Arg Phe Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala
        195                 200                 205

tcc cct gag ggc aaa gag ttc acc cga gac acg cac gtc ttc aca gga   672
Ser Pro Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly
    210                 215                 220

gag gtc acc ctg gac gcg tcg gct gtc tcc ctc ttc gac gac cac ctg   720
Glu Val Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu
225                 230                 235                 240

gga gag gac tac tat ggc agt gag atc tac acc cta aag gaa gga ctg   768
Gly Glu Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu
                245                 250                 255

tct tcc gtc cca caa ggg ctc cta cag gct ttt ctg gac gcc gca gac   816
Ser Ser Val Pro Gln Gly Leu Leu Gln Ala Phe Leu Asp Ala Ala Asp
            260                 265                 270

tcc aac gag ttc tat ccc aac agc cac ctg aag gcc ctg aga cgt aag   864
Ser Asn Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys
        275                 280                 285

acc aac ggt cag tat gtt ctt tac ttt gag ccc acc acc tcc aag gat   912
Thr Asn Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp
    290                 295                 300

gga caa acc aca atc aac tat ctg gaa ccc ctg cag gtt gtg tgt gca   960
Gly Gln Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala
305                 310                 315                 320

caa aga gtc atc ctg gcc atg ccg gta tac gct ctg aac caa cta gac  1008
Gln Arg Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp
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tgg aat cag ctc aga aat gac cga gcc acc caa gcg tac gct gcc gtt   1056
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cgc ccg att cct gca agt aag gtg ttc atg tcc ttt gat cag ccc tgg   1104
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tgg ttg gag aac gag agg aaa tcc tgg gtc acc aag tcg gac gcg ctt   1152
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    370                 375                 380


ttc agc caa atg tac gac tgg cag aag tct gag gcg tcc gga gac tac   1200
Phe Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr
385                 390                 395                 400

atc ctg atc gcc agc tac gcc gac ggc ctc aaa gcc cag tac ctg cgg   1248
Ile Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg
                405                 410                 415

gag ctg aag aat cag gga gag gac atc cca ggc tct gac cca ggc tac   1296
Glu Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr
            420                 425                 430

aac cag gtt acc gaa ccc ctc aag gac acc att ctt gac cac ctc act   1344
Asn Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr
        435                 440                 445

gag gct tat ggc gtg gag cga gac tcg atc ccg gaa ccc gtg acc gcc   1392
Glu Ala Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala
    450                 455                 460

gct tcc cag ttc tgg aca gac tac ccg ttt ggc tgt gga tgg atc acc   1440
Ala Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr
465                 470                 475                 480

tgg agg gcc ggc ttc cat ttc gat gac gtc atc agc acc atg cgt cgc   1488
Trp Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg
                485                 490                 495

ccg tca ctg aaa gat gag gta tac gtg gtg gga gcc gac tac tcc tgg   1536
Pro Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp
            500                 505                 510

gga ctt atc tcc tcc tgg ata gag ggc gct ctg gag acc tcg gaa aac   1584
Gly Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn
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Cys Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly
         35                  40                  45

Ala Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val
     50                  55                  60

Phe Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu
 65                  70                  75                  80

Pro Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile
                 85                  90                  95

Glu Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu
            100                 105                 110

Thr Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg
        115                 120                 125

Phe Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly
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Asp Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn
145                 150                 155                 160

Leu Val Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Gln Leu Asn Gly
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Glu Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly
            180                 185                 190

Arg Phe Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala
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Ser Pro Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly
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Glu Val Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu
225                 230                 235                 240

Gly Glu Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu
                245                 250                 255

Ser Ser Val Pro Gln Gly Leu Leu Gln Ala Phe Leu Asp Ala Ala Asp
            260                 265                 270

Ser Asn Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys
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        275                 280                 285

Thr Asn Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp
    290                 295                 300

Gly Gln Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala
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Gln Arg Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp
                325                 330                 335

Trp Asn Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val
            340                 345                 350

Arg Pro Ile Pro Ala Ser Lys Val Phe Met Ser Phe Asp Gln Pro Trp
        355                 360                 365

Trp Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu
    370                 375                 380

Phe Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr
385                 390                 395                 400

Ile Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg
                405                 410                 415

Glu Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr
            420                 425                 430

Asn Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr
        435                 440                 445

Glu Ala Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala
    450                 455                 460

Ala Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr
465                 470                 475                 480

Trp Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg
                485                 490                 495

Pro Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp
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Gly Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn
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Val Ile Asn Asp Tyr Phe Leu
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<213> Aplysia punctata

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  1               5                  10                  15

gcc gac ggt gtc tgc aga aac aga cgt caa tgt aac aga gag gtg tgc   96
Ala Asp Gly Val Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val Cys
             20                  25                  30

ggt tct acc tac gat gtg gcc gtc gtg ggg gcg ggg cct ggg gga gct  144
Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala
         35                  40                  45

aac tcc gcc tac atg ctg agg gac tcc ggc ctg gac atc gct gtg ttc  192
Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe
     50                  55                  60

gag tac tca gac cga gtg ggc ggc cgg ctg ttc acc tac cag ctg ccc  240
Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro
 65                  70                  75                  80

aac aca ccc gac gtt aat ctc gag att ggc ggc atg agg ttc atc gag  288
Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu
                 85                  90                  95

ggc gcc atg cac agg ctc tgg agg gtc att tca gaa ctc ggc cta acc  336
Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr
            100                 105                 110

ccc aag gtg ttc aag gaa ggt ttc gga aag gag ggc aga cag aga ttt  384
Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe
        115                 120                 125

tac ctg cgg gga cag agc ctg acc aag aaa cag gtc aag agt ggg gac  432
Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp
    130                 135                 140

gta ccc tat gac ctc agc ccg gag gag aaa gaa aac cag gga aat ctg  480
Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu
145                 150                 155                 160

gtc gaa tac tac ctg gag aaa ctg aca ggt cta caa ctc aat ggt gaa  528
Val Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Gln Leu Asn Gly Glu
                165                 170                 175

ccg ctc aaa cgt gag gtt gcg ctt aaa cta acc gtg ccg gac ggc aga  576
Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg
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            180                 185                 190

ttc ctc tat gac ctc tcg ttt gac gaa gcc atg gat ctg gtt gcc tcc   624
Phe Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser
        195                 200                 205

cct gag ggc aaa gag ttc acc cga gac acg cac gtc ttc acc gga gag   672
Pro Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu
    210                 215                 220

gtc acc ctg ggc gcg tcg gct gtc tcc ctc ttc gac gac cac ctg gga   720
Val Thr Leu Gly Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly
225                 230                 235                 240

gag gac tac tac ggc agt gag atc tac acc ctc aag gaa gga ctg tct   768
Glu Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser
                245                 250                 255

tcc gtc cct caa ggg ctc cta cag gct ttt ctg gac gcc gca gac tcc   816
Ser Val Pro Gln Gly Leu Leu Gln Ala Phe Leu Asp Ala Ala Asp Ser
            260                 265                 270

aac gag ttc tat ccc aac agc cac ctg aag gcc ctg aga cgt aag acc   864
Asn Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr
        275                 280                 285

aac ggt cag tat gtt ctt tac ttt gag ccc acc acc tcc aag gat gga   912
Asn Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly
    290                 295                 300

caa acc aca atc aac tat ctg gaa ccc ctg cag gtt gtg tgt gca cag   960
Gln Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln
305                 310                 315                 320

aga gtc att ctg gcc atg ccg gtc tac gct ctc aac cag ttg gat tgg  1008
Arg Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp
                325                 330                 335

aat cag ctc aga aat gac cga gcc acc caa gcg tac gct gcc gtg cgc  1056
Asn Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg
            340                 345                 350

ccg att cct gca agt aag gtg ttc atg acc ttt gat cag ccc tgg tgg  1104
Pro Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp
        355                 360                 365

ttg gag aac gag agg aaa tcc tgg gtc acc aag tcg gac gcg ctt ttc  1152
Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe
    370                 375                 380

agt caa atg tac gac tgg cag aag tct gag gcg tcc gga gac tac atc  1200
Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile
385                 390                 395                 400

ctg atc gcc agc tac gcc gac ggc ctc aaa gcc cag tac ctg cgg gag  1248
Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu
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                405                 410                 415

ctg aag aat cag gga gag gac atc cca ggc tct gac cca ggc tac aac   1296
Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn
            420                 425                 430

cag gtc acc gaa ccc ctc aag gac acc att ctt gac cac ctc act gag   1344
Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu
        435                 440                 445

gcc tat ggc gtg gag cga gac tcg atc cgg gaa ccc gtg acc gcc gct   1392
Ala Tyr Gly Val Glu Arg Asp Ser Ile Arg Glu Pro Val Thr Ala Ala
    450                 455                 460

tcc cag ttc tgg aca gac tac ccg ttt ggc tgt gga tgg atc acc tgg   1440
Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp
465                 470                 475                 480

agg gcc ggc ttc cat ttc gat gac gtc atc agc acc atg cgt cgc ccg   1488
Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro
                485                 490                 495

tca ctg aaa gat gag gtc tac gtg gtg gga gcc gat tac tcc tgg gga   1536
Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly
            500                 505                 510

ctt atc tcc tcc tgg ata gag ggc gct ctg gag acc tca gaa aac gtc   1584
Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val
        515                 520                 525

atc aac gac tac ttc ctc taa                                      1605
Ile Asn Asp Tyr Phe Leu
    530                 535
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<213> Aplysia punctata

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            20                  25                  30

Gly Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala
        35                  40                  45

Asn Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe
    50                  55                  60

Glu Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro
65                  70                  75                  80

Asn Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu
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                85                  90                  95

Gly Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr
            100                 105                 110

Pro Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe
        115                 120                 125

Tyr Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp
    130                 135                 140

Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu
145                 150                 155                 160

Val Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Gln Leu Asn Gly Glu
                165                 170                 175

Pro Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg
            180                 185                 190

Phe Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser
        195                 200                 205

Pro Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu
    210                 215                 220

Val Thr Leu Gly Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly
225                 230                 235                 240

Glu Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser
                245                 250                 255

Ser Val Pro Gln Gly Leu Leu Gln Ala Phe Leu Asp Ala Ala Asp Ser
            260                 265                 270

Asn Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr
        275                 280                 285

Asn Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly
    290                 295                 300

Gln Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln
305                 310                 315                 320

Arg Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp
                325                 330                 335

Asn Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg
            340                 345                 350

Pro Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp
        355                 360                 365

Leu Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe
    370                 375                 380
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```
Ser Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile
385                 390                 395                 400

Leu Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu
                405                 410                 415

Leu Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn
            420                 425                 430

Gln Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu
        435                 440                 445

Ala Tyr Gly Val Glu Arg Asp Ser Ile Arg Glu Pro Val Thr Ala Ala
    450                 455                 460

Ser Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp
465                 470                 475                 480

Arg Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro
                485                 490                 495

Ser Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly
            500                 505                 510

Leu Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val
        515                 520                 525

Ile Asn Asp Tyr Phe Leu
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  1               5                  10                  15

tct acc tac gat gtg gct gtc gtg ggg gcg ggg cct ggg gga gct aac   96
Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn
            20                  25                  30

tcc gcc tac atg ctg agg gac tcc ggc ctg gac atc gct gtg ttc gag  144
Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu
        35                  40                  45

tac tca gac cga gtg ggc ggc cgg ctg ttc acc tac cag ctg ccc aac  192
Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro Asn
    50                  55                  60
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aca ccc gac gtt aat ctc gag att ggc ggc atg agg ttc atc gag ggc   240
Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu Gly
 65                  70                  75                  80

gcc atg cac agg ctc tgg agg gtc att tca gaa ctc ggc cta acc ccc   288
Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr Pro
                 85                  90                  95

aag gtg ttc aag gaa ggt ttc gga aag gag ggc aga cag aga ttt tac   336
Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe Tyr
            100                 105                 110

ctg cgg gga cag agc ctg acc aag aaa cag gtc aag agt ggg gac gta   384
Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp Val
        115                 120                 125

ccc tat gac ctc agc ccg gag gag aaa gaa aac cag gga aat ctg gtc   432
Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu Val
    130                 135                 140

gaa tac tac ctg gag aaa ctg aca ggt cta aaa ctc aac ggc gga ccg   480
Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Lys Leu Asn Gly Gly Pro
145                 150                 155                 160

ctc aaa cgt gag gtt gcg ctt aaa cta acc gtg ccg gac ggc aga ttc   528
Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg Phe
                165                 170                 175

ctc tat gac ctc tcg ttt gac gaa gcc atg gac ctg gtt gcc tcc cct   576
Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser Pro
            180                 185                 190

gag ggc aaa gag ttc acc cga gac acg cac gtg ttc acc gga gaa gtc   624
Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu Val
        195                 200                 205

acc ctg gac gcg tcg gct gtc tcc ctc ttc gac gac cac ctg gga gag   672
Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly Glu
    210                 215                 220

gac tac tat ggc agt gag atc tac acc cta aag gaa gga ctg tct tcc   720
Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser Ser
225                 230                 235                 240

gtc cca caa ggg ctc cta cag act ttt ctg gac gcc gca gac tcc aac   768
Val Pro Gln Gly Leu Leu Gln Thr Phe Leu Asp Ala Ala Asp Ser Asn
                245                 250                 255

gag ttc tat ccc aac agc cac ctg aag gcc ctg aga cgt aag acc aac   816
Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr Asn
            260                 265                 270

ggt cag tat gtt ctt tac ttt gag ccc acc acc tcc aag gat gga caa   864
Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly Gln
        275                 280                 285
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acc aca atc aac tat ctg gaa ccc ctg cag gtt gtg tgt gca cag aga   912
Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln Arg
    290                 295                 300

gtc atc ctg gcc atg ccg gtc tac gct ctc aac caa ctg gac tgg aat   960
Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp Asn
305                 310                 315                 320

cag ctc aga aat gac cga gcc acc caa gcg tac gct gcc gtg cgc ccg   1008
Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro
                325                 330                 335

att cct gca agt aaa gtg ttc atg acc ttt gat cag ccc tgg tgg ttg   1056
Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu
            340                 345                 350

gag aac gag agg aaa tcc tgg gtc acc aag tcg gac gcg ctt ttc agc   1104
Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe Ser
        355                 360                 365

caa atg tac gac tgg cag aag tct gag gcg tcc gga gac tac atc ctg   1152
Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile Leu
    370                 375                 380

atc gcc agc tac gcc gac ggc ctc aaa gcc cag tac ctg cgg gag ctg   1200
Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu Leu
385                 390                 395                 400

aag aat cag gga gag gac atc cca ggc tct gac cca ggc tac aac cag   1248
Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn Gln
                405                 410                 415

gtc acc gaa ccc ctc aag gac acc att ctt gac cac ctc act gag gct   1296
Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu Ala
            420                 425                 430

tat ggc gtg gaa cga gac tcg atc ccg gaa ccc gtg acc gcc gct tcc   1344
Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala Ala Ser
        435                 440                 445

cag ttc tgg acc gac tac ccg ttc ggc tgt gga tgg atc acc tgg agg   1392
Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp Arg
    450                 455                 460

gca ggc ttc cat ttt gat gac gtc atc agc acc atg cgt cgc ccg tca   1440
Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro Ser
465                 470                 475                 480

ctg aaa gat gag gtc tac gtg gtg gga gcc gat tac tcc tgg gga ctt   1488
Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly Leu
                485                 490                 495

atc tcc tcc tgg ata gag ggc gct ctg gag acc tcg gaa aac gtc atc   1536
Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val Ile
            500                 505                 510

aac gac tac ttc ctc taa                                         1554
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Asn Asp Tyr Phe Leu
515

<210> 6
<211> 517
<212> PRT
<213> Aplysia punctata

<400> 6
Asp Gly Ile Cys Arg Asn Arg Arg Gln Cys Asn Arg Glu Val Cys Gly
1 5 10 15

Ser Thr Tyr Asp Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn
20 25 30

Ser Ala Tyr Met Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu
35 40 45

Tyr Ser Asp Arg Val Gly Gly Arg Leu Phe Thr Tyr Gln Leu Pro Asn
50 55 60

Thr Pro Asp Val Asn Leu Glu Ile Gly Gly Met Arg Phe Ile Glu Gly
65 70 75 80

Ala Met His Arg Leu Trp Arg Val Ile Ser Glu Leu Gly Leu Thr Pro
85 90 95

Lys Val Phe Lys Glu Gly Phe Gly Lys Glu Gly Arg Gln Arg Phe Tyr
100 105 110

Leu Arg Gly Gln Ser Leu Thr Lys Lys Gln Val Lys Ser Gly Asp Val
115 120 125

Pro Tyr Asp Leu Ser Pro Glu Glu Lys Glu Asn Gln Gly Asn Leu Val
130 135 140

Glu Tyr Tyr Leu Glu Lys Leu Thr Gly Leu Lys Leu Asn Gly Gly Pro
145 150 155 160

Leu Lys Arg Glu Val Ala Leu Lys Leu Thr Val Pro Asp Gly Arg Phe
165 170 175

Leu Tyr Asp Leu Ser Phe Asp Glu Ala Met Asp Leu Val Ala Ser Pro
180 185 190

Glu Gly Lys Glu Phe Thr Arg Asp Thr His Val Phe Thr Gly Glu Val
195 200 205

Thr Leu Asp Ala Ser Ala Val Ser Leu Phe Asp Asp His Leu Gly Glu
210 215 220

Asp Tyr Tyr Gly Ser Glu Ile Tyr Thr Leu Lys Glu Gly Leu Ser Ser
225 230 235 240

Val Pro Gln Gly Leu Leu Gln Thr Phe Leu Asp Ala Ala Asp Ser Asn
245 250 255

```
Glu Phe Tyr Pro Asn Ser His Leu Lys Ala Leu Arg Arg Lys Thr Asn
            260                 265                 270

Gly Gln Tyr Val Leu Tyr Phe Glu Pro Thr Thr Ser Lys Asp Gly Gln
        275                 280                 285

Thr Thr Ile Asn Tyr Leu Glu Pro Leu Gln Val Val Cys Ala Gln Arg
    290                 295                 300

Val Ile Leu Ala Met Pro Val Tyr Ala Leu Asn Gln Leu Asp Trp Asn
305                 310                 315                 320

Gln Leu Arg Asn Asp Arg Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro
                325                 330                 335

Ile Pro Ala Ser Lys Val Phe Met Thr Phe Asp Gln Pro Trp Trp Leu
            340                 345                 350

Glu Asn Glu Arg Lys Ser Trp Val Thr Lys Ser Asp Ala Leu Phe Ser
        355                 360                 365

Gln Met Tyr Asp Trp Gln Lys Ser Glu Ala Ser Gly Asp Tyr Ile Leu
    370                 375                 380

Ile Ala Ser Tyr Ala Asp Gly Leu Lys Ala Gln Tyr Leu Arg Glu Leu
385                 390                 395                 400

Lys Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gly Tyr Asn Gln
                405                 410                 415

Val Thr Glu Pro Leu Lys Asp Thr Ile Leu Asp His Leu Thr Glu Ala
            420                 425                 430

Tyr Gly Val Glu Arg Asp Ser Ile Pro Glu Pro Val Thr Ala Ala Ser
        435                 440                 445

Gln Phe Trp Thr Asp Tyr Pro Phe Gly Cys Gly Trp Ile Thr Trp Arg
    450                 455                 460

Ala Gly Phe His Phe Asp Asp Val Ile Ser Thr Met Arg Arg Pro Ser
465                 470                 475                 480

Leu Lys Asp Glu Val Tyr Val Val Gly Ala Asp Tyr Ser Trp Gly Leu
                485                 490                 495

Ile Ser Ser Trp Ile Glu Gly Ala Leu Glu Thr Ser Glu Asn Val Ile
            500                 505                 510

Asn Asp Tyr Phe Leu
        515
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<210> 7
<211> 600
<212> DNA

<213> Human

<220>
<221> CDS
<222> (1)..(600)

<400> 7

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atg tct tca gga aat gct aaa att ggg cac cct gcc ccc aac ttc aaa   48
Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys
  1               5                  10                  15

gcc aca gct gtt atg cca gat ggt cag ttt aaa gat atc agc ctg tct   96
Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser
             20                  25                  30

gac tac aaa gga aaa tat gtt gtg ttc ttc ttt tac cct ctt gac ttc   144
Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe
         35                  40                  45

acc ttt gtg tgc ccc acg gag atc att gct ttc agt gat agg gca gaa   192
Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu
     50                  55                  60

gaa ttt aag aaa ctc aac tgc caa gtg att ggt gct tct gtg gat tct   240
Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser
 65                  70                  75                  80

cac ttc tgt cat cta gca tgg gtc aat aca cct aag aaa caa gga gga   288
His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly
                 85                  90                  95

ctg gga ccc atg aac att cct ttg gta tca gac ccg aag cgc acc att   336
Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile
            100                 105                 110

gct cag gat tat ggg gtc tta aag gct gat gaa ggc atc tcg ttc agg   384
Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg
        115                 120                 125

ggc ctt ttt atc att gat gat aag ggt att ctt cgg cag atc act gta   432
Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val
    130                 135                 140

aat gac ctc cct gtt ggc cgc tct gtg gat gag act ttg aga cta gtt   480
Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val
145                 150                 155                 160

cag gcc ttc cag ttc act gac aaa cat ggg gaa gtg tgc cca gct ggc   528
Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
                165                 170                 175

tgg aaa cct ggc agt gat acc atc aag cct gat gtc caa aag agc aaa   576
Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys
            180                 185                 190

gaa tat ttc tcc aag cag aag tga                                  600
Glu Tyr Phe Ser Lys Gln Lys
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195 200

<210> 8
<211> 199
<212> PRT
<213> Human

<400> 8
Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn Phe Lys
1 5 10 15

Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser Leu Ser
20 25 30

Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe
35 40 45

Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu
50 55 60

Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser
65 70 75 80

His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln Gly Gly
85 90 95

Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg Thr Ile
100 105 110

Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser Phe Arg
115 120 125

Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile Thr Val
130 135 140

Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg Leu Val
145 150 155 160

Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro Ala Gly
165 170 175

Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys Ser Lys
180 185 190

Glu Tyr Phe Ser Lys Gln Lys
195

<210> 9
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic

double-stranded RNA molecule

<400> 9
ggcugaugaa ggcaucucg 19

<210> 10
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 10
augcuaaaau ugggcaccc 19

<210> 11
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 11
ugcuaaaauu gggcacccu 19

<210> 12
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 12
cuucaaagcc acagcuguu 19

<210> 13
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 13
agccacagcu guuaugcca 19

<210> 14
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 14
gccacagcug uuaugccag 19

<210> 15
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 15
agauaucagc cugucugac 19

<210> 16
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 16
gauaucagcc ugucugacu 19

<210> 17
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 17
gaaacucaac ugccaagug 19

<210> 18
<211> 19
<212> RNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 18
acucaacugc caagugauu 19

<210> 19
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 19
cucaacugcc aagugauug 19

<210> 20
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 20
cugccaagug auuggugcu 19

<210> 21
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 21
gugauuggug cuucugugg 19

<210> 22
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 22
gaaacaagga ggacuggga 19

<210> 23
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 23
cauuccuuug guaucagac 19

<210> 24
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 24
aggcugauga aggcaucuc 19

<210> 25
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 25
gcgcaccäuu gcucaggau 19

<210> 26
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 26
ggguauucuu cggcagauc 19

<210> 27
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 27
accuggcagu gauaccauc 19

<210> 28
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 28
ccuggcagug auaccauca 19

<210> 29
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 29
gccugauguc caaaagagc 19

<210> 30
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 30
cuggacuucc agaagaaca 19

<210> 31
<211> 19
<212> RNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic
double-stranded RNA molecule

<400> 31
cuuacgcuga guacuucga 19

<210> 32
<211> 7
<212> PRT
<213> Aplysia

<400> 32
Asp Gly Glu Asp Ala Ala Val
1 5

<210> 33
<211> 9
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (1)
<223> Asp can be Asp or Gln

<220>
<221> MOD_RES
<222> (3)
<223> Ile can be Ile or Val

<220>
<221> MOD_RES
<222> (7)
<223> Gln can be Gln or Arg

<220>
<221> MOD_RES
<222> (9)
<223> Pro can be Pro or Gln

<400> 33
Asp Gly Ile Cys Arg Asn Gln Arg Pro
1 5

<210> 34
<211> 4
<212> PRT
<213> Aplysia

<400> 34

Phe Ala Asp Ser
1

<210> 35
<211> 8
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (5)
<223> Ile can be Ile or Leu

<400> 35
Gly Pro Asp Gly Ile Val Ala Asp
1 5

<210> 36
<211> 7
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (6)
<223> Lys can be Lys or Gln

<220>
<221> MOD_RES
<222> (7)
<223> Ile can be Ile or Leu

<400> 36
Pro Gly Glu Val Ser Lys Ile
1 5

<210> 37
<211> 15
<212> PRT
<213> Aplysia

<400> 37
Ala Thr Gln Ala Tyr Ala Ala Val Arg Pro Ile Pro Ala Ser Lys
1 5 10 15

<210> 38
<211> 13
<212> PRT
<213> Aplysia

<400> 38
Asp Ser Gly Leu Asp Ile Ala Val Glu Tyr Ser Asp Arg
1 5 10

<210> 39
<211> 12
<212> PRT
<213> Aplysia

<400> 39
Gly Asp Val Pro Tyr Asp Leu Ser Pro Glu Glu Lys
1 5 10

<210> 40
<211> 442
<212> DNA
<213> Aplysia

<400> 40
caagacgggg aagacaagga gtttgacgga gaaatcgtca gcgtcagagt gctgaaggcg 60
ttcggcaagc ctggctacgg ttacaagcag ccctcgtgca aggaaggcaa ggactacgtg 120
agcagcggca gcgttcttca cgtgctgcag tgtgccggct tcttcgaggt gtgctacgag 180
gagaggatca ccacccagcc agccacgact gtcgctgcag cagaggtaca atgcaaaaag 240
ttcatcgcaa cccacaaatt ggaggagact gttgatggaa ggatcgtcag catcgagctt 300
gtccagagac tgaagaaaca atccggatac ggtccaagtg gcggttctgg ttatggcaac 360
ggtcatggtc aaagacccgg ttacggatac ggttctggta gtggaagtgg ctacgccccc 420
agaggaggat acaacccaaa ag 442

<210> 41
<211> 147
<212> PRT
<213> Aplysia

<400> 41
Gln Asp Gly Glu Asp Lys Glu Phe Asp Gly Glu Ile Val Ser Val Arg
1 5 10 15

Val Leu Lys Ala Phe Gly Lys Pro Gly Tyr Gly Tyr Lys Gln Pro Ser
20 25 30

Cys Lys Glu Gly Lys Asp Tyr Val Ser Ser Gly Ser Val Leu His Val
35 40 45

Leu Gln Cys Ala Gly Phe Phe Glu Val Cys Tyr Glu Glu Arg Ile Thr
50 55 60

Thr Gln Pro Ala Thr Thr Val Ala Ala Ala Glu Val Gln Cys Lys Lys
65 70 75 80

Phe Ile Ala Thr His Lys Leu Glu Glu Thr Val Asp Gly Arg Ile Val
85 90 95

```
Ser Ile Glu Leu Val Gln Arg Leu Lys Lys Gln Ser Gly Tyr Gly Pro
            100                 105                 110

Ser Gly Gly Ser Gly Tyr Gly Asn Gly His Gly Gln Arg Pro Gly Tyr
        115                 120                 125

Gly Tyr Gly Ser Gly Ser Gly Ser Gly Tyr Ala Pro Arg Gly Gly Tyr
    130                 135                 140

Asn Pro Lys
145
```

<210> 42
<211> 462
<212> DNA
<213> Aplysia

<400> 42
taccgccccc gccaccactn tngcaccagc agaaccaacc tgcgagaagc tgtccgtntg 60
gttcaacgtg ganaagaaat tcgaaggttc cagaatcgtg agtttcaagc tcatccgcct 120
gttcaacagg tncaagaagt gcaagaaagn ccagtattcc gtgtctggcg atgatgagga 180
cncattcgtt gtcagtggtt gttctggcgt gttccaggtn tgctacgaag aacaaacggc 240
gcccgctaca accnccacag aagccccgaa gccagagcca agaagaccca agaggaaaaa 300
ttccccaatc aaatttngta aacactgatg ggttaatntg acgaccagtg cgtctgcgaa 360
agaatcatgt tatggttcat gatgtcatgc tcttaatata ggttgtaacg tttaacgcga 420
tacagacatt aaaactcatt gttcaaaaaa aaaaaaaaaa aa 462

<210> 43
<211> 155
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (1)..(155)
<223> Xaa = unknown amino acid or STOP-codon

<400> 43
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Tyr Arg Pro Arg His His Xaa Xaa Thr Ser Arg Thr Asn Leu Arg Glu
  1               5                  10                  15

Ala Val Arg Xaa Val Gln Arg Gly Xaa Glu Ile Arg Arg Phe Gln Asn
            20                  25                  30

Arg Glu Phe Gln Ala His Pro Pro Val Gln Gln Xaa Gln Glu Val Gln
        35                  40                  45

Glu Xaa Pro Val Phe Arg Val Trp Arg Xaa Xaa Gly Xaa Ile Arg Cys
    50                  55                  60

Gln Trp Leu Phe Trp Arg Val Pro Gly Xaa Leu Arg Arg Thr Asn Gly
65                  70                  75                  80
```

```
Ala Arg Tyr Asn Xaa His Arg Ser Pro Glu Ala Arg Ala Lys Lys Thr
                  85                  90                  95

Gln Glu Glu Lys Phe Pro Asn Gln Ile Xaa Xaa Thr Leu Met Gly Xaa
            100                 105                 110

Xaa Asp Asp Gln Cys Val Cys Glu Arg Ile Met Leu Trp Phe Met Met
        115                 120                 125

Ser Cys Ser Xaa Xaa Tyr Arg Leu Xaa Arg Leu Thr Arg Tyr Arg His
    130                 135                 140

Xaa Asn Ser Leu Phe Lys Lys Lys Lys Lys Lys
145                 150                 155
```

<210> 44
<211> 153
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (1)..(153)
<223> Xaa = unknown amino acid or STOP-codon

<400> 44

```
Thr Ala Pro Ala Thr Thr Xaa Ala Pro Ala Glu Pro Thr Cys Glu Lys
  1               5                  10                  15

Leu Ser Xaa Trp Phe Asn Val Xaa Lys Lys Phe Glu Gly Ser Arg Ile
            20                  25                  30

Val Ser Phe Lys Leu Ile Arg Leu Phe Asn Arg Xaa Lys Lys Cys Lys
        35                  40                  45

Lys Xaa Gln Tyr Ser Val Ser Gly Asp Asp Glu Asp Xaa Phe Val Val
     50                  55                  60

Ser Gly Cys Ser Gly Val Phe Gln Xaa Cys Tyr Glu Glu Gln Thr Ala
 65                  70                  75                  80

Pro Ala Thr Thr Xaa Thr Glu Ala Pro Lys Pro Glu Pro Arg Arg Pro
                 85                  90                  95

Lys Arg Lys Asn Phe Pro Ile Lys Phe Xaa Lys His Xaa Trp Val Asn
            100                 105                 110

Xaa Thr Thr Ser Ala Ser Ala Lys Glu Ser Cys Tyr Gly Ser Xaa Cys
        115                 120                 125

His Ala Leu Asn Ile Gly Cys Asn Val Xaa Arg Asp Thr Asp Ile Lys
    130                 135                 140

Thr His Cys Ser Lys Lys Lys Lys Lys
145                 150
```

<210> 45
<211> 153
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (1)..(153)
<223> Xaa = unknown amino acid or STOP-codon

<400> 45
Pro Pro Pro Pro Pro Xaa Xaa His Gln Gln Asn Gln Pro Ala Arg Ser
1 5 10 15

Cys Pro Xaa Gly Ser Thr Trp Xaa Arg Asn Ser Lys Val Pro Glu Ser
20 25 30

Xaa Val Ser Ser Ser Ser Ala Cys Ser Thr Gly Xaa Arg Ser Ala Arg
35 40 45

Lys Xaa Ser Ile Pro Cys Leu Ala Met Met Arg Xaa His Ser Leu Ser
50 55 60

Val Val Val Leu Ala Cys Ser Arg Xaa Ala Thr Lys Asn Lys Arg Arg
65 70 75 80

Pro Leu Gln Xaa Pro Gln Lys Pro Arg Ser Gln Ser Gln Glu Asp Pro
85 90 95

Arg Gly Lys Ile Ser Gln Ser Asn Xaa Val Asn Thr Asp Gly Leu Xaa
100 105 110

Xaa Arg Pro Val Arg Leu Arg Lys Asn His Val Met Val His Asp Val
115 120 125

Met Leu Leu Ile Xaa Val Val Thr Phe Asn Ala Ile Gln Thr Leu Lys
130 135 140

Leu Ile Val Gln Lys Lys Lys Lys Lys
145 150

<210> 46
<211> 9
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (3)
<223> Ile can be Ile or Val

<400> 46

Asp Gly Ile Cys Arg Asn Arg Arg Gln
1 5

<210> 47
<211> 14
<212> PRT
<213> Aplysia

<400> 47
Asp Ser Gly Leu Asp Ile Ala Val Phe Glu Tyr Ser Asp Arg
1 5 10

<210> 48

<211> 7
<212> PRT
<213> Aplysia

<400> 48
Val Phe Glu Tyr Ser Asp Arg
1 5

<210> 49
<211> 16
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = any amino acid, in particular Thr

<400> 49
Leu Phe Xaa Tyr Gln Leu Pro Asn Thr Pro Asp Val Asn Leu Glu Ile
1 5 10 15

<210> 50
<211> 10
<212> PRT
<213> Aplysia

<400> 50
Val Ile Ser Glu Leu Gly Leu Thr Pro Lys
1 5 10

<210> 51
<211> 11

<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (5)
<223> Xaa = any amino acid, in particular Met

<400> 51
Val Ile Leu Ala Xaa Pro Val Tyr Ala Leu Asn
1 5 10

<210> 52
<211> 8
<212> PRT
<213> Aplysia

<400> 52
Val Phe Met Thr Phe Asp Gln Pro
1 5

<210> 53
<211> 10
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (6)
<223> Phe can be Phe or Ser

<400> 53
Ser Asp Ala Leu Phe Phe Gln Met Tyr Asp
1 5 10

<210> 54
<211> 18
<212> PRT
<213> Aplysia

<400> 54
Ser Glu Ala Ser Gly Asp Tyr Ile Leu Ile Ala Ser Tyr Ala Asp Gly
1 5 10 15

Leu Lys

<210> 55

<211> 21
<212> PRT
<213> Aplysia

<220>
<221> MOD_RES
<222> (12)
<223> Gln can be Gln or Gly

<400> 55
Asn Gln Gly Glu Asp Ile Pro Gly Ser Asp Pro Gln Tyr Asn Gln Val
1 5 10 15

Thr Glu Pro Leu Lys
20

<210> 56
<211> 28
<212> PRT
<213> Aplysia

<400> 56
Val Ala Val Val Gly Ala Gly Pro Gly Gly Ala Asn Ser Ala Tyr Met
1 5 10 15

Leu Arg Asp Ser Gly Leu Asp Ile Ala Val Phe Glu
20 25

<210> 57
<211> 8
<212> PRT
<213> Aplysia

<400> 57
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